

**Amendments to the Specification**

**Please replace the paragraph beginning at page of this page 2, line 23, with the following amended paragraph:**

In *Arabidopsis thaliana*, seven P<sub>1B</sub>-ATPases were previously identified (Axelsen and Palmgren, 2001) but the recent genome release revealed an eighth gene belonging to the HMAs group (P-type ATPase database; <http://biobase.dk/~axe/Pathbase.html>)).

**Please replace the paragraph beginning at page of this page 6, line 3, with the following amended paragraph:**

According to the invention, said P<sub>1B</sub>-type ATPase is preferably of eukaryotic origin, and more preferably from a higher plant. In a preferred embodiment, said P<sub>1B</sub>-type ATPase is selected amongst HMA1, HMA2, HMA3 and HMA4. When the wild-type plant to be genetically modified for phytoremediation possesses HMA gene(s), additional copies of at least one of said endogenous gene(s) is (are) preferably introduced into said plant genome, in order of overexpress said endogenous gene(s). Alternatively, for example in case the wild-type plant is defective for the P<sub>1B</sub>-type ATPase, the expression of which is desired in said plant for achieving phytoremediation of heavy metals, said P<sub>1B</sub>-type ATPase can be selected from the group consisting of heavy metal ATPase HMA1 to HMA4 of *Arabidopsis thaliana* (i.e., AtHMA1, AtHMA2, AtHMA3 and AtHMA4), whatever the ecotype, or from another plant species. ~~The corresponding sequences of *Arabidopsis thaliana* are available on the following websites: <http://mips.gsf.de> or <http://biobase.dk/~axe/Pathbase.html>.~~

**Please replace the paragraph beginning at page of this page 10, line 30, with the following amended paragraph:**

- **Figure 1:** Nucleic and amino acid sequences of AtHMA4 from the Ws ecotype (accession number AF412407 SEQ ID NOs:23 and 24). The grey highlighted characters correspond to the 5' UTR. The N-terminal heavy metal motif, the numerous cysteine doublets and the His stretch are boxed; the highly conserved sites are underlined. The amino acid sequence deleted in the alternative spliced form is black highlighted. The position of the stop insertion for the *Athma4ΔHis* form and its GFP fusion is indicated by the solid black vertical arrow while the empty one corresponds to the GFP fusion position of *AtHMA4* and *Athma4as*.